

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: ARMITAGE, RICHARD
FANSLOW, WILLIAM
SPRIGGS, MELANIE
SRINIVASAN, SUBHASHINI
GIBSON, MARYLOU
- (ii) TITLE OF INVENTION: NOVEL CYTOKINE
- (iii) NUMBER OF SEQUENCES: 23
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: IMMUNEX CORPORATION
 - (B) STREET: 51 UNIVERSITY STREET
 - (C) CITY: SEATTLE
 - (D) STATE: WASHINGTON
 - (E) COUNTRY: USA
 - (F) ZIP: 98101
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: Apple Macintosh
 - (C) OPERATING SYSTEM: Apple Operating System 7.1
 - (D) SOFTWARE: Microsoft Word for Apple, version 5.1a
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 07/969,703
 - (B) FILING DATE: October 23, 1992
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 07/805,723
 - (B) FILING DATE: December 5, 1991
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 07/783,707
 - (B) FILING DATE: October 25, 1991
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Perkins, Patricia A.
 - (B) REGISTRATION NUMBER: 34,693
 - (C) REFERENCE/DOCKET NUMBER: 2802-C
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 2065870430
 - (B) TELEFAX: 2065870606

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 783 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: MOUSE

(vii) IMMEDIATE SOURCE:

(B) CLONE: CD40-L

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..783

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG ATA GAA ACA TAC AGC CAA CCT TCC CCC AGA TCC GTG GCA ACT GGA
48
Met Ile Glu Thr Tyr Ser Gln Pro Ser Pro Arg Ser Val Ala Thr Gly
1 5 10 15

CTT CCA GCG AGC ATG AAG ATT TTT ATG TAT TTA CTT ACT GTT TTC CTT
96
Leu Pro Ala Ser Met Lys Ile Phe Met Tyr Leu Leu Thr Val Phe Leu
20 25 30

ATC ACC CAA ATG ATT GGA TCT GTG CTT TTT GCT GTG TAT CTT CAT AGA
144
Ile Thr Gln Met Ile Gly Ser Val Leu Phe Ala Val Tyr Leu His Arg
35 40 45

AGA TTG GAT AAG GTC GAA GAG GAA GTA AAC CTT CAT GAA GAT TTT GTA
192
Arg Leu Asp Lys Val Glu Glu Glu Val Asn Leu His Glu Asp Phe Val
50 55 60

TTC ATA AAA AAG CTA AAG AGA TGC AAC AAA GGA GAA GGA TCT TTA TCC
240
Phe Ile Lys Lys Leu Lys Arg Cys Asn Lys Gly Glu Gly Ser Leu Ser
65 70 75 80

TTG CTG AAC TGT GAG GAG ATG AGA AGG CAA TTT GAA GAC CTT GTC AAG
288
Leu Leu Asn Cys Glu Glu Met Arg Arg Gln Phe Glu Asp Leu Val Lys
85 90 95

GAT ATA ACG TTA AAC AAA GAA GAG AAA AAA GAA AAC AGC TTT GAA ATG
 336
 Asp Ile Thr Leu Asn Lys Glu Glu Lys Lys Glu Asn Ser Phe Glu Met
 100 105 110

CAA AGA GGT GAT GAG GAT CCT CAA ATT GCA GCA CAC GTT GTA AGC GAA
 384
 Gln Arg Gly Asp Glu Asp Pro Gln Ile Ala Ala His Val Val Ser Glu
 115 120 125

GCC AAC AGT AAT GCA GCA TCC GTT CTA CAG TGG GCC AAG AAA GGA TAT
 432
 Ala Asn Ser Asn Ala Ala Ser Val Leu Gln Trp Ala Lys Lys Gly Tyr
 130 135 140

TAT ACC ATG AAA AGC AAC TTG GTA ATG CTT GAA AAT GGG AAA CAG CTG
 480
 Tyr Thr Met Lys Ser Asn Leu Val Met Leu Glu Asn Gly Lys Gln Leu
 145 150 155 160

ACG GTT AAA AGA GAA GGA CTC TAT TAT GTC TAC ACT CAA GTC ACC TTC
 528
 Thr Val Lys Arg Glu Gly Leu Tyr Tyr Val Tyr Thr Gln Val Thr Phe
 165 170 175

TGC TCT AAT CGG GAG CCT TCG AGT CAA CGC CCA TTC ATC GTC GGC CTC
 576
 Cys Ser Asn Arg Glu Pro Ser Ser Gln Arg Pro Phe Ile Val Gly Leu
 180 185 190

TGG CTG AAG CCC AGC AGT GGA TCT GAG AGA ATC TTA CTC AAG GCG GCA
 624
 Trp Leu Lys Pro Ser Ser Gly Ser Glu Arg Ile Leu Leu Lys Ala Ala
 195 200 205

AAT ACC CAC AGT TCC TCC CAG CTT TGC GAG CAG CAG TCT GTT CAC TTG
 672
 Asn Thr His Ser Ser Ser Gln Leu Cys Glu Gln Gln Ser Val His Leu
 210 215 220

GGC GGA GTG TTT GAA TTA CAA GCT GGT GCT TCT GTG TTT GTC AAC GTG
 720
 Gly Gly Val Phe Glu Leu Gln Ala Gly Ala Ser Val Phe Val Asn Val
 225 230 235 240

ACT GAA GCA AGC CAA GTG ATC CAC AGA GTT GGC TTC TCA TCT TTT GGC
 768
 Thr Glu Ala Ser Gln Val Ile His Arg Val Gly Phe Ser Ser Phe Gly
 245 250 255

TTA CTC AAA CTC TGA
 783
 Leu Leu Lys Leu
 260

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 260 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ile Glu Thr Tyr Ser Gln Pro Ser Pro Arg Ser Val Ala Thr Gly
 1 5 10 15
 Leu Pro Ala Ser Met Lys Ile Phe Met Tyr Leu Leu Thr Val Phe Leu
 20 25 30
 Ile Thr Gln Met Ile Gly Ser Val Leu Phe Ala Val Tyr Leu His Arg
 35 40 45
 Arg Leu Asp Lys Val Glu Glu Glu Val Asn Leu His Glu Asp Phe Val
 50 55 60
 Phe Ile Lys Lys Leu Lys Arg Cys Asn Lys Gly Glu Gly Ser Leu Ser
 65 70 75 80
 Leu Leu Asn Cys Glu Glu Met Arg Arg Gln Phe Glu Asp Leu Val Lys
 85 90 95
 Asp Ile Thr Leu Asn Lys Glu Glu Lys Lys Glu Asn Ser Phe Glu Met
 100 105 110
 Gln Arg Gly Asp Glu Asp Pro Gln Ile Ala Ala His Val Val Ser Glu
 115 120 125
 Ala Asn Ser Asn Ala Ala Ser Val Leu Gln Trp Ala Lys Lys Gly Tyr
 130 135 140
 Tyr Thr Met Lys Ser Asn Leu Val Met Leu Glu Asn Gly Lys Gln Leu
 145 150 155 160
 Thr Val Lys Arg Glu Gly Leu Tyr Tyr Val Tyr Thr Gln Val Thr Phe
 165 170 175
 Cys Ser Asn Arg Glu Pro Ser Ser Gln Arg Pro Phe Ile Val Gly Leu
 180 185 190
 Trp Leu Lys Pro Ser Ser Gly Ser Glu Arg Ile Leu Leu Lys Ala Ala
 195 200 205
 Asn Thr His Ser Ser Ser Gln Leu Cys Glu Gln Gln Ser Val His Leu
 210 215 220
 Gly Gly Val Phe Glu Leu Gln Ala Gly Ala Ser Val Phe Val Asn Val
 225 230 235 240
 Thr Glu Ala Ser Gln Val Ile His Arg Val Gly Phe Ser Ser Phe Gly
 245 250 255
 Leu Leu Lys Leu

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 740 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: HUMAN

(vii) IMMEDIATE SOURCE:
 (B) CLONE: IgG1 Fc

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGGTACCGCT AGCGTCGACA GGCCTAGGAT ATCGATACGT AGAGCCCAGA TCTTGTGACA
60
AAACTCACAC ATGCCCACCG TGCCAGCAC CTGAACTCCT GGGGGGACCG TCAGTCTTCC
120
TCTTCCCCC AAAACCCAAG GACACCCTCA TGATCTCCCG GACCCCTGAG GTCACATGCG
180
TGGTGGTGGA CGTGAGCCAC GAAGACCCTG AGGTCAAGTT CAACTGGTAC GTGGACGGCG
240
TGGAGGTGCA TAATGCCAAG ACAAAGCCGC GGGAGGAGCA GTACAACAGC ACGTACCGGG
300
TGGTCAGCGT CCTCACCGTC CTGCACCAGG ACTGGCTGAA TGGCAAGGAC TACAAGTGCA
360
AGGTCTCCAA CAAAGCCCTC CCAGCCCCCA TGCAGAAAAC CATCTCCAA GCCAAAGGGC
420
AGCCCCGAGA ACCACAGGTG TACACCCTGC CCCATCCCG GGATGAGCTG ACCAAGAACC
480
AGGTCAGCCT GACCTGCCTG GTCAAAGGCT TCTATCCAG GCACATCGCC GTGGAGTGGG
540
AGAGCAATGG GCAGCCGGAG AACAACTACA AGACCACGCC TCCCGTGCTG GACTCCGACG
600
GCTCCTTCTT CCTCTACAGC AAGCTCACCG TGGACAAGAG CAGGTGGCAG CAGGGGAACG
660

TCTTCTCATG CTCCGTGATG CATGAGGCTC TGCACAACCA CTACACGCAG AAGAGCCTCT
720

CCCTGTCTCC GGGTAAATGA
740

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: HUMAN

(vii) IMMEDIATE SOURCE:

(B) CLONE: CD40 EXTRACELLULAR REGION

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CAGAACCACC CACTGCATGC AGAGAAAAC AGTACCTAAT AAACAGTCAG TGCTGTTCTT
60

TGTGCCAGCC AGGACAGAAA CTGGTGAGTG ACTGCACAGA GTTCACTGAA ACGGAATGCC
120

TTCCTTGCGG TGAAAGCGAA TTCCTAGACA CCTGGAACAG AGAGACACAC TGCCACCAGC
180

ACAAATACTG CGACCCCAAC CTAGGGCTTC GGGTCCAGCA GAAGGGCACC TCAGAAACAG
240

ACACCATCTG CACCTGTGAA GAAGGCTGGC ACTGTACGAG TGAGGCCTGT GAGAGCTGTG
300

TCCTGCACCG CTCATGCTCG CCCGGCTTTG GGGTCAAGCA GATTGCTACA GGGGTTTCTG
360

ATACCATCTG CGAGCCCTGC CCAGTCGGCT TCTTCTCCAA TGTGTCATCT GCTTTCGAAA
420

AATGTCACCC TTGGACAAGC TGTGAGACCA AAGACCTGGT TGTGCAACAG GCAGGCACAA
480

ACAAGACTGA TGTTGTCTGT GGTCCCCAGG ATCGGCTGA
519

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PCR PRIMER
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: CD40 5' PRIMER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCGTCGACCA CCATGGTTCG TCTGCC
26

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PCR PRIMER
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: CD40 3' PRIMER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCGTCGACGT CTAGAGCCGA TCCTGGGG
28

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PCR PRIMER

(vii) IMMEDIATE SOURCE:

(B) CLONE: CD40 3' DOWNSTREAM PRIMER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ACAAGATCTG GGCTCTACGT ACTCAGCCGA TCCTGGGGAC
40

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PENTAPEPTIDE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Tyr Val Gly Pro Arg
1 5

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PCR PRIMER

(vii) IMMEDIATE SOURCE:

(B) CLONE: HUMAN IGG1/FC 5' PRIMER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TATTAATCAT TCAGTAGGGC CCAGATCTTG TGACAAAAC CAC
43

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PCR PRIMER

(vii) IMMEDIATE SOURCE:

(B) CLONE: HUMAN IGG1/FC 3' DOWNSTREAM PRIMER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCCAGCTTAA CTAGTTCATT TACCCGAGA CAGGGAGA
38

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 840 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

(B) CLONE: CD40-L

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 46..831

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr Phe Cys Ser
 165 170 175
 AAT CGG GAA GCT TCG AGT CAA GCT CCA TTT ATA GCC AGC CTC TGC CTA
 630
 Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser Leu Cys Leu
 180 185 190 195
 AAG TCC CCC GGT AGA TTC GAG AGA ATC TTA CTC AGA GCT GCA AAT ACC
 678
 Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala Ala Asn Thr
 200 205 210
 CAC AGT TCC GCC AAA CCT TGC GGG CAA CAA TCC ATT CAC TTG GGA GGA
 726
 His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His Leu Gly Gly
 215 220 225
 GTA TTT GAA TTG CAA CCA GGT GCT TCG GTG TTT GTC AAT GTG ACT GAT
 774
 Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn Val Thr Asp
 230 235 240
 CCA AGC CAA GTG AGC CAT GGC ACT GGC TTC ACG TCC TTT GGC TTA CTC
 822
 Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu Leu
 245 250 255
 AAA CTC TGAACAGTGT CA
 840
 Lys Leu
 260

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 261 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Ile Glu Thr Tyr Asn Gln Thr Ser Pro Arg Ser Ala Ala Thr Gly
 1 5 10 15
 Leu Pro Ile Ser Met Lys Ile Phe Met Tyr Leu Leu Thr Val Phe Leu
 20 25 30
 Ile Thr Gln Met Ile Gly Ser Ala Leu Phe Ala Val Tyr Leu His Arg
 35 40 45
 Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu His Glu Asp Phe Val
 50 55 60
 Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser Leu Ser

65

70

75

80

Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe Val Lys
 85 90 95
 Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser Phe Glu
 100 105 110
 Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser
 115 120 125
 Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly
 130 135 140
 Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln
 145 150 155 160
 Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr
 165 170 175
 Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser
 180 185 190
 Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala
 195 200 205
 Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His
 210 215 220
 Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn
 225 230 235 240
 Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe
 245 250 255
 Gly Leu Leu Lys Leu
 260

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TAT ATG TTC CAT GTT TCT TTT AGA TAT ATC TTT GGA ATT CCT CCA CTG
48
Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Ile Pro Pro Leu
-25 -20 -15

ATC CTT GTT CTG CTG CCT GTC ACT AGC TCT GAC TAC AAA GAT GAC GAT
96
Ile Leu Val Leu Leu Pro Val Thr Ser Ser Asp Tyr Lys Asp Asp Asp
-10 -5 1 5

GAT AAA AGA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA
144
Asp Lys Arg Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
10 15 20

CCT GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC
192
Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
25 30 35

AAG GAC ACC CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG
240
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
40 45 50

GTG GAC GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG
288
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
55 60 65 70

GAC GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG CGG GAG GAG CAG
336
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
75 80 85

TAC AAC AGC ACG TAC CGG GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG
384
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
90 95 100

GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GCC
432
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
105 110 115

CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC
480
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
120 125 130

CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG ACC
528
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
135 140 145 150

AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC
 576
 Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 155 160 165

GAC ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC
 624
 Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 170 175 180

AAG ACC ACG CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC
 672
 Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 185 190 195

AGC AAG CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC
 720
 Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 200 205 210

TCA TGC TCC GTG ATG CAT GGT GGC GGA GGG TCA GGC GGA GGT GGG TCC
 768
 Ser Cys Ser Val Met His Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 215 220 225 230

GGA GGC GGG GGT TCA AGT TCT GAC AAG ATA GAA GAT GAA AGG AAT CTT
 816
 Gly Gly Gly Gly Ser Ser Ser Asp Lys Ile Glu Asp Glu Arg Asn Leu
 235 240 245

CAT GAA GAT TTT GTA TTC ATG AAA ACG ATA CAG AGA TGC AAC ACA GGA
 864
 His Glu Asp Phe Val Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly
 250 255 260

GAA AGA TCC TTA TCC TTA CTG AAC TGT GAG GAG ATT AAA AGC CAG TTT
 912
 Glu Arg Ser Leu Ser Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe
 265 270 275

GAA GGC TTT GTG AAG GAT ATA ATG TTA AAC AAA GAG GAG ACG AAG AAA
 960
 Glu Gly Phe Val Lys Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys
 280 285 290

GAA AAC AGC TTT GAA ATG CAA AAA GGT GAT CAG AAT CCT CAA ATT GCG
 1008
 Glu Asn Ser Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala
 295 300 305 310

GCA CAT GTC ATA AGT GAG GCC AGC AGT AAA ACA ACA TCT GTG TTA CAG
 1056
 Ala His Val Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln
 315 320 325

TGG GCT GAA AAA GGA TAC TAC ACC ATG AGC AAC AAC TTG GTA ACC CTG
 1104
 Trp Ala Glu Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu

576
 624
 672
 720
 768
 816
 864
 912
 960
 1008
 1056
 1104

330

335

340

GAA AAT GGG AAA CAG CTG ACC GTT AAA AGA CAA GGA CTC TAT TAT ATC
1152

Glu Asn Gly Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile
345 350 355

TAT GCC CAA GTC ACC TTC TGT TCC AAT CGG GAA GCT TCG AGT CAA GCT
1200

Tyr Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala
360 365 370

CCA TTT ATA GCC AGC CTC TGC CTA AAG TCC CCC GGT AGA TTC GAG AGA
1248

Pro Phe Ile Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg
375 380 385 390

ATC TTA CTC AGA GCT GCA AAT ACC CAC AGT TCC GCC AAA CCT TGC GGG
1296

Ile Leu Leu Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly
395 400 405

CAA CAA TCC ATT CAC TTG GGA GGA GTA TTT GAA TTG CAA CCA GGT GCT
1344

Gln Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala
410 415 420

TCG GTG TTT GTC AAT GTG ACT GAT CCA AGC CAA GTG AGC CAT GGC ACT
1392

Ser Val Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly Thr
425 430 435

GGC TTC ACG TCC TTT GGC TTA CTC AAA CTC TGA
1425

Gly Phe Thr Ser Phe Gly Leu Leu Lys Leu
440 445

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 473 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Ile Pro Pro Leu Ile
-25 -20 -15 -10

Leu Val Leu Leu Pro Val Thr Ser Ser Asp Tyr Lys Asp Asp Asp Asp
-5 1 5

Lys Arg Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
10 15 20

[illegible]

330

335

340

Asn Gly Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr
 345 350 355
 Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro
 360 365 370 375
 Phe Ile Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile
 380 385 390
 Leu Leu Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln
 395 400 405
 Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser
 410 415 420
 Val Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly
 425 430 435
 Phe Thr Ser Phe Gly Leu Leu Lys Leu
 440 445

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 33 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Arg Met Lys Gln Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile
 1 5 10 15
 Tyr His Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu
 20 25 30

Arg

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 55 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATATGAATTC GACTACAAAG ATGACGATGA TAAACCTCAA ATTGCAGCAC ACGTT
21

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CCTTCGCGGC CGCGTTCAGA GTTTGAGTAA GCCAA
35

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 929 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Human CD40-L trimer

(ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 65..142

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 65..886

(ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 143..886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TGAGCGAGTC CGCATCGACG GATCGGAAAA CCTCTCCGAG GTACCTATCC CGGGGATCCC

CACC	ATG	TTC	CAT	GTT	TCT	TTT	AGA	TAT	ATC	TTT	GGA	ATT	CCT	CCA	CTG	109
Met	Phe	His	Val	Ser	Phe	Arg	Tyr	Ile	Phe	Gly	Ile	Pro	Pro	Leu		
-26	-25					-20					-15					
ATC	CTT	GTT	CTG	CTG	CCT	GTC	ACT	AGT	TCT	GAC	CGT	ATG	AAA	CAG	ATA	157
Ile	Leu	Val	Leu	Leu	Pro	Val	Thr	Ser	Ser	Asp	Arg	Met	Lys	Gln	Ile	
-10						-5					1				5	
GAG	GAT	AAG	ATC	GAA	GAG	ATC	CTA	AGT	AAG	ATT	TAT	CAT	ATA	GAG	AAT	205
Glu	Asp	Lys	Ile	Glu	Glu	Ile	Leu	Ser	Lys	Ile	Tyr	His	Ile	Glu	Asn	
				10					15					20		
GAA	ATC	GCC	CGT	ATC	AAA	AAG	CTG	ATT	GGC	GAG	CGG	ACT	AGT	TCT	GAC	253
Glu	Ile	Ala	Arg	Ile	Lys	Lys	Leu	Ile	Gly	Glu	Arg	Thr	Ser	Ser	Asp	
			25					30					35			
AAG	ATA	GAA	GAT	GAA	AGG	AAT	CTT	CAT	GAA	GAT	TTT	GTA	TTC	ATG	AAA	301
Lys	Ile	Glu	Asp	Glu	Arg	Asn	Leu	His	Glu	Asp	Phe	Val	Phe	Met	Lys	
		40					45					50				
ACG	ATA	CAG	AGA	TGC	AAC	ACA	GGA	GAA	AGA	TCC	TTA	TCC	TTA	CTG	AAC	349
Thr	Ile	Gln	Arg	Cys	Asn	Thr	Gly	Glu	Arg	Ser	Leu	Ser	Leu	Leu	Asn	
	55					60					65					
TGT	GAG	GAG	ATT	AAA	AGC	CAG	TTT	GAA	GGC	TTT	GTG	AAG	GAT	ATA	ATG	397
Cys	Glu	Glu	Ile	Lys	Ser	Gln	Phe	Glu	Gly	Phe	Val	Lys	Asp	Ile	Met	
70				75						80					85	
TTA	AAC	AAA	GAG	GAG	ACG	AAG	AAA	GAA	AAC	AGC	TTT	GAA	ATG	CAA	AAA	445
Leu	Asn	Lys	Glu	Glu	Thr	Lys	Lys	Glu	Asn	Ser	Phe	Glu	Met	Gln	Lys	
				90					95					100		
GGT	GAT	CAG	AAT	CCT	CAA	ATT	GCG	GCA	CAT	GTC	ATA	AGT	GAG	GCC	AGC	493
Gly	Asp	Gln	Asn	Pro	Gln	Ile	Ala	Ala	His	Val	Ile	Ser	Glu	Ala	Ser	
			105					110					115			
AGT	AAA	ACA	ACA	TCT	GTG	TTA	CAG	TGG	GCT	GAA	AAA	GGA	TAC	TAC	ACC	541
Ser	Lys	Thr	Thr	Ser	Val	Leu	Gln	Trp	Ala	Glu	Lys	Gly	Tyr	Tyr	Thr	
		120					125					130				
ATG	AGC	AAC	AAC	TTG	GTA	ACC	CTG	GAA	AAT	GGG	AAA	CAG	CTG	ACC	GTT	589
Met	Ser	Asn	Asn	Leu	Val	Thr	Leu	Glu	Asn	Gly	Lys	Gln	Leu	Thr	Val	
	135					140					145					
AAA	AGA	CAA	GGA	CTC	TAT	TAT	ATC	TAT	GCC	CAA	GTC	ACC	TTC	TGT	TCC	637
Lys	Arg	Gln	Gly	Leu	Tyr	Tyr	Ile	Tyr	Ala	Gln	Val	Thr	Phe	Cys	Ser	
150					155					160					165	
AAT	CGG	GAA	GCT	TCG	AGT	CAA	GCT	CCA	TTT	ATA	GCC	AGC	CTC	TGC	CTA	685
Asn	Arg	Glu	Ala	Ser	Ser	Gln	Ala	Pro	Phe	Ile	Ala	Ser	Leu	Cys	Leu	
				170					175					180		
AAG	TCC	CCC	GGT	AGA	TTC	GAG	AGA	ATC	TTA							

His	Ser	Ser	Ala	Lys	Pro	Cys	Gly	Gln	Gln	Ser	Ile	His	Leu	Gly	Gly	
		200					205					210				
GTA	TTT	GAA	TTG	CAA	CCA	GGT	GCT	TCG	GTG	TTT	GTC	AAT	GTG	ACT	GAT	829
Val	Phe	Glu	Leu	Gln	Pro	Gly	Ala	Ser	Val	Phe	Val	Asn	Val	Thr	Asp	
	215					220					225					
CCA	AGC	CAA	GTG	AGC	CAT	GGC	ACT	GGC	TTC	ACG	TCC	TTT	GGC	TTA	CTC	877
Pro	Ser	Gln	Val	Ser	His	Gly	Thr	Gly	Phe	Thr	Ser	Phe	Gly	Leu	Leu	
230					235					240				245		
AAA	CTC	TGAGCGGCCG	CTACAGATGA	ATAATAAGCA	TGTTTGGATT	CCTCAA										929
Lys	Leu															

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 273 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met	Phe	His	Val	Ser	Phe	Arg	Tyr	Ile	Phe	Gly	Ile	Pro	Pro	Leu	Ile	
-26	-25					-20					-15					
Leu	Val	Leu	Leu	Pro	Val	Thr	Ser	Ser	Asp	Arg	Met	Lys	Gln	Ile	Glu	
-10					-5					1				5		
Asp	Lys	Ile	Glu	Glu	Ile	Leu	Ser	Lys	Ile	Tyr	His	Ile	Glu	Asn	Glu	
			10					15					20			
Ile	Ala	Arg	Ile	Lys	Lys	Leu	Ile	Gly	Glu	Arg	Thr	Ser	Ser	Asp	Lys	
		25					30					35				
Ile	Glu	Asp	Glu	Arg	Asn	Leu	His	Glu	Asp	Phe	Val	Phe	Met	Lys	Thr	
	40					45					50					
Ile	Gln	Arg	Cys	Asn	Thr	Gly	Glu	Arg	Ser	Leu	Ser	Leu	Leu	Asn	Cys	
55					60					65				70		
Glu	Glu	Ile	Lys	Ser	Gln	Phe	Glu	Gly	Phe	Val	Lys	Asp	Ile	Met	Leu	
				75					80					85		
Asn	Lys	Glu	Glu	Thr	Lys	Lys	Glu	Asn	Ser	Phe	Glu	Met	Gln	Lys	Gly	
			90					95					100			
Asp	Gln	Asn	Pro	Gln	Ile	Ala	Ala	His	Val	Ile	Ser	Glu	Ala	Ser	Ser	
		105				110						115				
Lys	Thr	Thr	Ser	Val	Leu	Gln	Trp	Ala	Glu	Lys	Gly	Tyr	Tyr	Thr	Met	
	120					125					130					
Ser	Asn	Asn	Leu	Val	Thr	Leu	Glu	Asn	Gly	Lys	Gln	Leu	Thr	Val	Lys	

135		140		145		150									
Arg	Gln	Gly	Leu	Tyr	Tyr	Ile	Tyr	Ala	Gln	Val	Thr	Phe	Cys	Ser	Asn
				155					160					165	
Arg	Glu	Ala	Ser	Ser	Gln	Ala	Pro	Phe	Ile	Ala	Ser	Leu	Cys	Leu	Lys
			170					175					180		
Ser	Pro	Gly	Arg	Phe	Glu	Arg	Ile	Leu	Leu	Arg	Ala	Ala	Asn	Thr	His
		185					190					195			
Ser	Ser	Ala	Lys	Pro	Cys	Gly	Gln	Gln	Ser	Ile	His	Leu	Gly	Gly	Val
	200					205					210				
Phe	Glu	Leu	Gln	Pro	Gly	Ala	Ser	Val	Phe	Val	Asn	Val	Thr	Asp	Pro
215				220					225						230
Ser	Gln	Val	Ser	His	Gly	Thr	Gly	Phe	Thr	Ser	Phe	Gly	Leu	Leu	Lys
				235					240				245		

Leu

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 878 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 - (B) CLONE: Murine CD40-L trimer
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: 15..92
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 15..857
- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 93..857

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CTCGAGGTAC	CGCC	ATG	TTC	CAT	GTT	TCT	TTT	AGA	TAT	ATC	TTT	GGA	ATT	50	
		Met	Phe	His	Val	Ser	Phe	Arg	Tyr	Ile	Phe	Gly	Ile		
		-26	-25					-20				-15			
CCT	CCA	CTG	ATC	CTT	GTT	CTG	CTG	CCT	GTC	ACT	AGT	TCT	GAC	CGT	ATG
Pro	Pro	Leu	Ile	Leu	Val	Leu	Leu	Pro	Val	Thr	Ser	Ser	Asp	Arg	Met
				-10				-5						1	98

AAA Lys	CAG Gln	ATA Ile	GAG Glu	GAT Asp	AAG Lys	ATC Ile	GAA Glu	GAG Glu	ATC Ile	CTA Leu	AGT Ser	AAG Lys	ATT Ile	TAT Tyr	CAT His	146
		5					10					15				
ATA Ile	GAG Glu	AAT Asn	GAA Glu	ATC Ile	GCC Ala	CGT Arg	ATC Ile	AAA Lys	AAG Lys	CTG Leu	ATT Ile	GGC Gly	GAG Glu	CGG Arg	ACT Thr	194
	20					25					30					
AGT Ser	TCT Ser	GAC Asp	TAC Tyr	AAA Lys	GAT Asp	GAC Asp	GAT Asp	GAT Asp	AAA Lys	GAT Asp	AAG Lys	GTC Val	GAA Glu	GAG Glu	GAA Glu	242
	35				40					45					50	
GTA Val	AAC Asn	CTT Leu	CAT His	GAA Glu	GAT Asp	TTT Phe	GTA Val	TTC Phe	ATA Ile	AAA Lys	AAG Lys	CTA Leu	AAG Lys	AGA Arg	TGC Cys	290
				55					60					65		
AAC Asn	AAA Lys	GGA Gly	GAA Glu	GGA Gly	TCT Ser	TTA Leu	TCC Ser	TTG Leu	CTG Leu	AAC Asn	TGT Cys	GAG Glu	GAG Glu	ATG Met	AGA Arg	338
			70					75					80			
AGG Arg	CAA Gln	TTT Phe	GAA Glu	GAC Asp	CTT Leu	GTC Val	AAG Lys	GAT Asp	ATA Ile	ACG Thr	TTA Leu	AAC Asn	AAA Lys	GAA Glu	GAG Glu	386
		85					90					95				
AAA Lys	AAA Lys	GAA Glu	AAC Asn	AGC Ser	TTT Phe	GAA Glu	ATG Met	CAA Gln	AGA Arg	GGT Gly	GAT Asp	GAG Glu	GAT Asp	CCT Pro	CAA Gln	434
	100					105					110					
ATT Ile	GCA Ala	GCA Ala	CAC His	GTT Val	GTA Val	AGC Ser	GAA Glu	GCC Ala	AAC Asn	AGT Ser	AAT Asn	GCA Ala	GCA Ala	TCC Ser	GTT Val	482
	115				120					125					130	
CTA Leu	CAG Gln	TGG Trp	GCC Ala	AAG Lys	AAA Lys	GGA Gly	TAT Tyr	TAT Tyr	ACC Thr	ATG Met	AAA Lys	AGC Ser	AAC Asn	TTG Leu	GTA Val	530
				135					140					145		
ATG Met	CTT Leu	GAA Glu	AAT Asn	GGG Gly	AAA Lys	CAG Gln	CTG Leu	ACG Thr	GTT Val	AAA Lys	AGA Arg	GAA Glu	GGA Gly	CTC Leu	TAT Tyr	578
			150					155					160			
TAT Tyr	GTC Val	TAC Tyr	ACT Thr	CAA Gln	GTC Val	ACC Thr	TTC Phe	TGC Cys	TCT Ser	AAT Asn	CGG Arg	GAG Glu	CCT Pro	TCG Ser	AGT Ser	626
		165					170					175				
CAA Gln	CGC Arg	CCA Pro	TTC Phe	ATC Ile	GTC Val	GGC Gly	CTC Leu	TGG Trp	CTG Leu	AAG Lys	CCC Pro	AGC Ser	AGT Ser	GGA Gly	TCT Ser	674
	180					185					190					
GAG Glu	AGA Arg	ATC Ile	TTA Leu	CTC Leu	AAG Lys	GCG Ala	GCA Ala	AAT Asn	ACC Thr	CAC His	AGT Ser	TCC Ser	TCC Ser	CAG Gln	CTT Leu	722
	195				200					205					210	
TGC Cys	GAG Glu	CAG Gln	CAG Gln	TCT Ser	GTT Val	CAC His	TTG Leu	GGC Gly	GGA Gly	GTG Val	TTT Phe	GAA Glu	TTA Leu	CAA Gln	GCT Ala	770
				215					220					225		
GGT Gly	GCT Gly	TCT Gly	GTG Gly	TTT Gly	GTC Gly	AAC Gly	GTG Gly	ACT Gly	GAA Gly	GCA Gly	AGC Gly	CAA Gly	GTG Gly	ATC Gly	CAC Gly	818

Gly Ala Ser Val Phe Val Asn Val Thr Glu Ala Ser Gln Val Ile His
 230 235 240

AGA GTT GGC TTC TCA TCT TTT GGC TTA CTC AAA CTC TGAACGCGGC
 Arg Val Gly Phe Ser Ser Phe Gly Leu Leu Lys Leu
 245 250 255

864

CGCTACAGAT CTAC

878

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 280 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Ile Pro Pro Leu Ile
 -26 -25 -20 -15
 Leu Val Leu Leu Pro Val Thr Ser Ser Asp Arg Met Lys Gln Ile Glu
 -10 -5 1 5
 Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile Tyr His Ile Glu Asn Glu
 10 15 20
 Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu Arg Thr Ser Ser Asp Tyr
 25 30 35
 Lys Asp Asp Asp Asp Lys Asp Lys Val Glu Glu Glu Val Asn Leu His
 40 45 50
 Glu Asp Phe Val Phe Ile Lys Lys Leu Lys Arg Cys Asn Lys Gly Glu
 55 60 65 70
 Gly Ser Leu Ser Leu Leu Asn Cys Glu Glu Met Arg Arg Gln Phe Glu
 75 80 85
 Asp Leu Val Lys Asp Ile Thr Leu Asn Lys Glu Glu Lys Lys Glu Asn
 90 95 100
 Ser Phe Glu Met Gln Arg Gly Asp Glu Asp Pro Gln Ile Ala Ala His
 105 110 115
 Val Val Ser Glu Ala Asn Ser Asn Ala Ala Ser Val Leu Gln Trp Ala
 120 125 130
 Lys Lys Gly Tyr Tyr Thr Met Lys Ser Asn Leu Val Met Leu Glu Asn
 135 140 145 150
 Gly Lys Gln Leu Thr Val Lys Arg Glu Gly Leu Tyr Tyr Val Tyr Thr
 155 160 165
 Gln Val Thr Phe Cys Ser Asn Arg Glu Pro Ser Ser Gln Arg Pro Phe

170

175

180

Ile Val Gly Leu Trp Leu Lys Pro Ser Ser Gly Ser Glu Arg Ile Leu
185 190 195

Leu Lys Ala Ala Asn Thr His Ser Ser Ser Gln Leu Cys Glu Gln Gln
200 205 210

Ser Val His Leu Gly Gly Val Phe Glu Leu Gln Ala Gly Ala Ser Val
215 220 225 230

Phe Val Asn Val Thr Glu Ala Ser Gln Val Ile His Arg Val Gly Phe
235 240 245

Ser Ser Phe Gly Leu Leu Lys Leu
250

170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250